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PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/786,926

DATE: 07/27/2001
 TIME: 19:54:31

ENTERED

Input Set : A:\ES.txt
 Output Set: N:\CRF3\07272001\I786926.raw

3 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
 5 <120> TITLE OF INVENTION: Human and murine G-protein coupled EDG6 receptor
 6 (endothelial differentiation gene) and use of same
 8 <130> FILE REFERENCE: 101195-45
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/786,926
 11 <141> CURRENT FILING DATE: 2001-03-09
 13 <150> PRIOR APPLICATION NUMBER: DE 198 43 240.2
 14 <151> PRIOR FILING DATE: 1998-09-11
 16 <150> PRIOR APPLICATION NUMBER: DE 198 46 979.9
 17 <151> PRIOR FILING DATE: 1998-10-13
 19 <150> PRIOR APPLICATION NUMBER: PCT/DE 99/02871
 20 <151> PRIOR FILING DATE: 1999-09-10
 22 <160> NUMBER OF SEQ ID NOS: 4
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 384
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: human
 33 G-protein-coupled EDG6 receptor
 35 <400> SEQUENCE: 1
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 40 20 25 30
 42 Gly Arg Leu Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala
 43 35 40 45
 45 Leu Arg Gly Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn
 46 50 55 60
 48 Leu Leu Val Leu Ala Ala Ile Thr Ser His Met Arg Ser Arg Arg Trp
 49 65 70 75 80
 51 Val Tyr Tyr Cys Leu Val Asn Ile Thr Leu Ser Asp Leu Leu Thr Gly
 52 85 90 95
 54 Ala Ala Tyr Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg
 55 100 105 110
 57 Leu Ala Pro Ala Gln Trp Phe Leu Arg Glu Gly Leu Leu Phe Thr Ala
 58 115 120 125
 60 Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Glu Arg Phe
 61 130 135 140
 63 Ala Thr Met Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser
 64 145 150 155 160
 66 Arg Val Tyr Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu
 67 165 170 175
 69 Gly Met Leu Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg
 70 180 185 190
 72 Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys

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75 Leu Val Ile Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly
76          210          215          220
78 Ala Ile Phe Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro
79 225          230          235          240
81 Ala Ala Arg Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile
82          245          250          255
84 Leu Leu Ala Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Leu
85          260          265          270
87 Ala Asp Val Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly
88          275          280          285
90 Met Asp Trp Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro
91          290          295          300
93 Ile Ile Tyr Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser
94 305          310          315          320
96 Phe Leu Cys Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp
97          325          330          335
99 Cys Leu Ala Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp
100          340          345          350
102 Ser Ser Leu Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser
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115 <212> TYPE: DNA
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125 ccgagggatg gcggcctggg ggccctgcgg gggctgtcgg tggccgccag ctgcctggtg 180
126 gtgctggaga acttgctggt gctggcggcc atcaccagcc acatgcggtc gcgacgtgg 240
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128 gccaacgtgc tgetgtcggg ggeccgcacc ttccgtctgg cgcccgccca gtggttccta 360
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137 tgggccagag agtacctgcg gggcatggac tggatcctgg ccctggccgt cctcaactcg 900
138 gcggtcaacc ccatcatcta ctcttcgcg agcagggagg tgtgcagagc cgtgctcagc 960
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162 ttacagccg gcgagcgctt cgccaccatg gtgcgggtgg ctgagagtgg ggccaccaag 480
163 accagccgtg tgtatggctg catcggtctg tgctggctac tggcagctat cctgggcctg 540
164 ctgcccctgc tgggctggaa ctgtgtgtgc gccttccac gctgctccag cctgctgccc 600
165 ctctactoca agggctatgt gctcttttgt gtggtggtct tcgccctcat cctagtggct 660
166 atctgagcc tctacggggc catctttaga gtggtccgag ccaatgggca gaagtctcca 720
167 cgtcctctg cccgccgcaa gtcccgcagg ctactcaaca ccgtgctgat gatcttggtg 780
168 gcctttgtgg tgtgctgggg tcccctgttt ggctgctcc tggctgacat ctttggttct 840
169 aatgtctggg cccaggagta cctgctgtgc atggactgga tcctggccct ggccgtgttc 900
170 aactcagcca ttaatcctct catctactcc ttccgcagcc gtgaggtgca gcgcgctgtg 960
171 ctggccttcc tgtgctgcgg ctgtctctgg ctaggctctg gaggtccagg agactgctg 1020
172 acccgatca ccgaggccca ctccggtgca tccaccactg acagctccct gaggcccagg 1080
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177 <210> SEQ ID NO: 4
178 <211> LENGTH: 386
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: murine
184 G-protein-coupled EDG6 receptor
186 <400> SEQUENCE: 4
187 Met Asn Ile Ser Thr Trp Ser Thr Leu Val Thr Pro Glu Ser Cys His
188 1 5 10 15
190 Arg Leu Ala Ala Ser Gly His Ser Leu Leu Ile Val Leu His Tyr Asn
191 20 25 30
193 His Ser Gly Arg Leu Ala Ser Arg Gly Gly Ser Glu Asp Gly Gly Gly
194 35 40 45
196 Leu Gly Met Leu Arg Gly Pro Ser Val Ala Ala Gly Cys Leu Val Val
197 50 55 60
199 Leu Glu Asn Ala Met Val Leu Ala Ala Ile Ala Ile Tyr Met Arg Ser
200 65 70 75 80
202 Arg Arg Trp Val Tyr Tyr Cys Leu Leu Asn Ile Thr Leu Ser Asp Leu

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205 Leu Thr Gly Leu Ala Tyr Val Val Asn Val Leu Leu Ser Gly Thr Arg
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208 Thr Phe Gln Leu Ser Pro Val His Trp Phe Leu Arg Glu Gly Leu Leu
209          115          120          125
211 Phe Met Ala Leu Ala Ala Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly
212          130          135          140
214 Glu Arg Phe Ala Thr Met Val Arg Val Ala Glu Ser Gly Ala Thr Lys
215 145          150          155          160
217 Thr Ser Arg Val Tyr Gly Cys Ile Gly Leu Cys Trp Leu Leu Ala Ala
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220 Ile Leu Gly Leu Leu Pro Leu Leu Gly Trp Asn Cys Val Cys Ala Phe
221          180          185          190
223 Pro Arg Cys Ser Ser Leu Leu Pro Leu Tyr Ser Lys Gly Tyr Val Leu
224          195          200          205
226 Phe Cys Val Val Val Phe Ala Leu Ile Leu Val Ala Ile Leu Ser Leu
227          210          215          220
229 Tyr Gly Ala Ile Phe Arg Val Val Arg Ala Asn Gly Gln Lys Ser Pro
230 225          230          235          240
232 Arg Pro Pro Ala Arg Arg Lys Ser Arg Arg Leu Leu Asn Thr Val Leu
233          245          250          255
235 Met Ile Leu Val Ala Phe Val Val Cys Trp Gly Pro Leu Phe Gly Leu
236          260          265          270
238 Leu Leu Ala Asp Ile Phe Gly Ser Asn Val Trp Ala Gln Glu Tyr Leu
239          275          280          285
241 Arg Gly Met Asp Trp Ile Leu Ala Leu Ala Val Phe Asn Ser Ala Ile
242          290          295          300
244 Asn Pro Leu Ile Tyr Ser Phe Arg Ser Arg Glu Val Gln Arg Ala Val
245 305          310          315          320
247 Leu Ala Phe Leu Cys Cys Gly Cys Leu Trp Leu Gly Leu Arg Gly Pro
248          325          330          335
250 Gly Asp Cys Leu Thr Arg Ile Thr Glu Ala His Ser Gly Ala Ser Thr
251          340          345          350
253 Thr Asp Ser Ser Leu Arg Pro Arg Asp Ser Phe Arg Thr Ser Arg Ser
254          355          360          365
256 Leu Ser Phe Arg Met Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg
257          370          375          380
259 Ser Thr
260 385

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number